

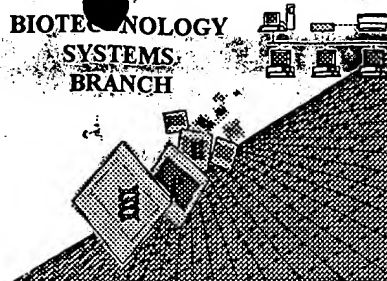


M-1-E

01/00 0280  
4-24-01

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

**RAW SEQUENCE LISTING  
ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/805,694

Source: OIPF

Date Processed by STIC: 4/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer-Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/805694

- NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**
- 1 \_\_\_\_\_ Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  - 2 \_\_\_\_\_ Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  - 3 \_\_\_\_\_ Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
  - 4 \_\_\_\_\_ Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
  - 5 \_\_\_\_\_ Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
  - 6 \_\_\_\_\_ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
  - 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  - 8 \_\_\_\_\_ Skipped Sequences (OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
  - 9 \_\_\_\_\_ Skipped Sequences (NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
  - 10 \_\_\_\_\_ Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  - 11 \_\_\_\_\_ Use of "Artificial" (NEW RULES)  
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
  - 12 \_\_\_\_\_ Use of <220>Feature (NEW RULES)  
Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
  - 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.



OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/805,694

DATE: 04/05/2001  
TIME: 08:05:50

Input Set : A:\BB1432 US NA Seq Listing.txt  
Output Set: N:\CRF3\04052001\I805694.raw

**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Kinney, Anthony  
5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans  
7 <130> FILE REFERENCE: BB1432 US NA  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/805,694  
C--> 10 <141> CURRENT FILING DATE: 2001-03-14  
12 <150> PRIOR APPLICATION NUMBER: 60/189,823  
W--> 13 <151> PRIOR FILING DATE: 16 MARCH 2000 2000-03-16  
15 <160> NUMBER OF SEQ ID NOS: 16  
17 <170> SOFTWARE: Microsoft Office 97

#### ERRORED SEQUENCES

230 <210> SEQ ID NO: 5  
231 <211> LENGTH: 494  
232 <212> TYPE: DNA  
233 <213> ORGANISM: Glycine max  
235 <400> SEQUENCE: 5  
E--> 236 acacagctng cacatattac atacacgtga atcactaatt aagccatgga gaagaaatca 60  
237 atagctgggt tgtgcttccct ctctcttggt ctctttggtg ctcaagaagt tgtggtgcaa 120  
238 actgaggcaa agacttgcca gaacctggct gatcacataga ggggtccatg cttcaccact 180  
239 ggcagctgcg atgacactcg caagaacaaa gagcacttgc tcagaggcag atgcagggac 240  
240 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300  
241 agatgcatgc agcgcatttt tataaaaaat acaactacta tatactatat ataataagac 360  
E--> 242 tgggcgctgc atcaatgacc ctatgtanta ttttatatat tattaccgat gtcaagaact 420  
E--> 243 atagatgcat gtactgtgca taacggctga gttatgtcon tangttanga ataaaaataa 480  
244 agtgcgtgtg ttgc 494

*see item 10  
on Error  
Summary Sheet*



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/805,694

DATE: 04/05/2001

TIME: 08:05:52

Input Set : A:\BB1432 US NA Seq Listing.txt

Output Set: N:\CRF3\04052001\I805694.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:236 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
M:340 Repeated in SeqNo=5



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

ANTHONY J. KINNEY ET AL.

# 4

CASE NO.: BB1432 US NA

APPLICATION NO.: 09/805,694

GROUP ART UNIT: UNKNOWN

FILED: MARCH 14, 2001

EXAMINER: UNKNOWN

FOR: HYPOALLERGENIC TRANSGENIC  
SOYBEANS

**STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)**

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

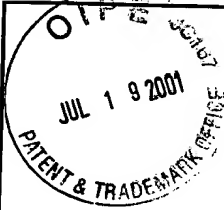
The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,

Lynne M. Christenbury  
Attorney For Applicants  
Registration No. 30,971  
Telephone: 302-992-5481  
Facsimile: 302-892-1026

Dated: July 16, 2001

sld



## Certificate of Mailing under 37 CFR 1.8

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to:

Assistant Commissioner for Patents  
Washington, D.C. 20231

on July 16, 2001  
Date

Susan L. Durkee  
Signature

SUSAN L. DURKEE  
Type or printed name of person signing Certificate

Note: Each paper must have its own certificate of mailing, or this certificate must identify each submitted paper.

09/805,694  
BB 1432 US NA  
FEE TRANSMITTAL  
STATEMENT UNDER 37 CFR 1.821 (g) and 1.825 (b)  
SEQ. LIST - 10 PAGES  
SEQ. LIST - CRF  
DECLARATION - R. JUNG  
DECLARATION - A. KINNEY  
POA - R. JUNG  
POA - A. KINNEY  
NOTICE TO FILE MISSING PARTS  
RAW SEQUENCE LISTING ERROR REPORT  
RESPONSE TO NOTICE TO FILE MISSING PARTS OF APPLICATION DATE GRANTED